

REMARKS

Claims 1-7, 12, 31 and 44-46 are pending. Claims 1, 4, 31 and 44 have been amended. Claims 8-11, 13-30 and 32-43 have been canceled. No new matter has been added.

Rejection of Claims 1-7, 12, 31 and 44-46 Under 35 U.S.C. §101

Claims 1-7, 12, 31 and 44-46 are rejected under 35 U.S.C. §101 “because the invention is not supported by a credible substantial, specific or well established utility.” According to the Examiner,

the art acknowledges that function cannot be predicted based solely on structural similarity of a known protein, and proteins of a same family, sharing a high degree of sequence similarity, may have diverse, and sometimes even opposite biological activities and functions. ... The present specification does not disclose any functional property or biological significance that is directly associated with human TANGO405, and further research to identify such is required, which renders the invention not substantial.

Applicants respectfully traverse this rejection. Contrary to the Examiner's assertions, the Applicant has provided sufficient evidence to establish that human TANGO 405 is a lectin ortholog of dectin-2 and has similar biological activity to dectin-2. In fact, the information provided in the present application regarding TANGO405 is very similar to that provided in Example 10 of the USPTO Training Material for the Revised Interim Utility Guidelines (hereafter referred to as the “Training Materials”) in which it was found that a “well established utility” was given. Applicants provide the following chart that compares the information provided in Example 10 of the Training Materials to that provided for the claimed invention.

Example 10	TANGO405
1) cDNA library was prepared from human kidney epithelial cells	1) cDNA library was prepared from a mixed lymphocyte reaction
2) The specification discloses ...that SEQ ID NO:2 has a high level of homology to a DNA ligase	2) The present application teaches that TANGO405 has 89% sequence homology with dectin-2
3) The specification teaches that this complete	3) The present application teaches the complete

ORF (SEQ ID NO:2) encodes SEQ ID NO:3	ORF (SEQ ID NO:52) of human TANGO405
4) Alignment of SEQ ID NO:3 with known amino acid sequences of DNA ligases indicates there is a high level of sequence conservation between various known ligases	4) A BLAST of the amino acid sequence of TANGO405 (Exhibit A) indicates that TANGO405 has a high level of homology with many known C-type lectin family members (including dectin-2 and isoforms thereof) and not with other non-C-type lectin family members
5) A search of prior art confirms that ...the next highest level of homology is alpha lectin. However, the latter homology is only 50%	5) A BLAST of the amino acid sequence of TANGO405 (Exhibit A) shows that the next highest level of homology with a non-C-type lectin protein is with an Fc-epsilon receptor III, with a homology of only 35.8%.
6) The overall <i>sequence similarity</i> between SEQ ID NO:3 and the consensus sequence of the known DNA ligases... reveals a similarity score of 95% (emphasis added)	6) The overall <i>sequence identity</i> between dectin-2 and TANGO405 is 89%. In addition, TANGO405 shows high levels <i>sequence similarity</i> with other C-type lectin family members (e.g., 76% <i>sequence similarity</i> with C-type lectin superfamily member 10)
	7) Both dectin-2 and TANGO405 include a single C-type lectin domain at the COOH terminus (which share a high level of sequence identity)
	8) TANGO405 contains C-type lectin domain signature
	9) A frameshift in the murine TANGO405 sequence results in the sequence of dectin-2

Thus, Applicants have provided more information regarding human TANGO405 than what was needed to demonstrate a credible substantial, specific or well established utility according to Example 10 of the Training Materials. The data in the present application provides sufficient evidence to establish that human TANGO 405 is a human ortholog of dectin-2 having similar biological activity.

Furthermore, as noted above, both human TANGO 405 and dectin-2 have a single C-type lectin domain in the COOH terminus. As shown in figure 4, the C-type lectin domain of human TANGO 405 is about 73% identical to the C-type lectin domain of dectin-2. This is a significantly higher level of identity within the C-type lectin domain of dectin-2 than seen with

other C-type lectins. See, e.g., Ariizumi et al. (2000) J. Biol. Chem. 275(16):11957-11963, page 11959 which provides that "the CRD domain in the dectin-2 polypeptide exhibited marked homology with the CRD sequences in other C-type lectins, such as DCIR (44.7%), MGL (43.8%), HL2 (45.8%)" In addition, the COOH-terminal region of both dectin-2 and human TANGO 405 contain all thirteen invariant amino acid residues conserved in the C-type lectin domain of many C-lectins. These high levels of sequence identity in a conserved relevant domain of dectin-2 provides further evidence that murine dectin-2 and human TANGO 405 have similar biological function.

In view of the above, it is clear that Applicants have provided sufficient data to establish a substantial credible utility for the claimed nucleic acid molecules. Therefore, Applicants respectfully request that the Examiner withdraw this rejection.

Rejection of Claims 1-7, 12, 31 and 44-46 Under 35 U.S.C. §112, first paragraph

Claims 1-7, 12, 31 and 44-46 are rejected under 35 U.S.C. §112, first paragraph.

Specifically, the Examiner has maintained the argument that "since the claimed invention is not supported by either a credible asserted utility or a well established utility for the reasons set forth above, one skilled in the art would not know how to use the claimed invention."

Applicants respectfully traverse this rejection. As discussed above in response to the utility rejection, the claimed invention does have a credible asserted utility, and as such one of skill in the art would be able to make and use the claimed invention.

The Examiner further asserts that even though "human TANGO405 and mouse dectin-2 may not share 40 nucleic acids or 15 amino acids with 100% sequence identity, ... there is no way to predict whether the human TANGO405 may share sequence identity with other unknown proteins having a distinct functional property." Further, the Examiner states that "it is well known in the art that it does not take 100% sequence identity for two molecule to hybridize, and therefore, without specifying regions specific for the human TANGO405 polynucleotide, a

randomly selected fragment of nucleotides from human TANGO405 polypeptide are likely to bind other molecules such as that encoding dectin-2.”

Applicants respectfully traverse this rejection. Several of the claims recite that nucleic acid molecules include at least 40 consecutive nucleic acid residues of the recited sequence or encode a fragment of a polypeptide having at least 15 consecutive amino acids of the recited sequences. Nucleic acid molecules of these lengths are specific to human TANGO 405, as compared to, e.g., dectin-2. As pointed out previously, under certain stringency conditions, probes and primers comprising the claimed nucleic acid fragments would hybridize only to human TANGO 405 polynucleotides. The Examiner seems to be requiring that the probes or primers hybridize under any conditions to only TANGO405. This is not required for the claimed nucleic acid fragments to be useful. Under certain high stringency conditions, nucleic acid fragments of the recited lengths are specific to TANGO405. Moreover, the Examiner has provided absolutely no evidence that the recited nucleic acid fragments would bind other “unknown proteins”. The Examiner appears to be speculating that somewhere out there, there may be a protein-yet to be discovered-that could be encoded by a nucleic acid having at least 40 consecutive residues of the recited nucleic acid sequence

Applicants also note that claim 2 recites a nucleic acid molecule that encodes at least the open reading frame of TANGO405. Claim 45 recites a nucleic acid molecule that includes at least 600 consecutive residues of sequence encoding TANGO405, or that encodes a polypeptide having at least 200 consecutive residues of TANGO405. Nucleic acids of these lengths are clearly specific to human TANGO405.

For the reasons discussed above, Applicants respectfully request that the Examiner withdraw this rejection.

Rejection of Claims 4 and 44 Under 35 U.S.C. §112, second paragraph

Claims 4 and 44 are rejected under 35 U.S.C. §112, second paragraph, “as being indefinite for failing to particularly point out and distinctly claim the subject matter which the

applicant regards as the invention.” In particular, the Examiner states that “claim 4 remains indefinite because ... it is unclear what the structural relationship of the heterologous polypeptide with said polypeptide, and whether the two nucleic acids are encoding a fusion protein or two separate proteins.”

Applicants respectfully traverse this rejection. Claim 4 is directed to a nucleic acid that includes a sequence encoding TANGO405 or a portion thereof and a sequence encoding a heterologous protein, i.e., a non-TANGO405 protein. The claim recites one nucleic acid molecule that includes both sequences. Thus, the structural relationship of the two nucleic acid sequences, one encoding TANGO405 and the other encoding a non-TANGO405 protein, is clear. They are contained within the same nucleic acid molecule. Whether the polypeptides encoded by the two sequences are fused or expressed as two separate proteins is not relevant, as the claim is directed to a nucleic acid, and the relationship of the elements of the nucleic acid are clear. Therefore, Applicants respectfully request that the Examiner withdraw this rejection.

With regard to claim 44, the Examiner asserts that “it is unclear what ‘a polypeptide’ is meant, and the host may produce polypeptides other than the polypeptides encoded by the transformed or transfected expression vector.”

Claim 44 has been amended to recite “a polypeptide encoded by a nucleic acid of claim 1”, thereby obviating this rejection.

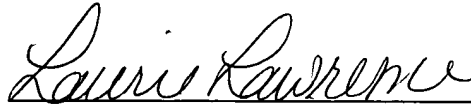
Applicant : McCarthy et al.
Serial No. : 09/766,511
Filed : January 19, 2001
Page : 11 of 11

Attorney's Docket No.: 10448-209001 / MPI00-
537OMNI

Enclosed is a check for the Petition for Extension of Time fee. Please apply any other charges or credits to deposit account 06-1050.

Respectfully submitted,

Date: 3/23/04


Laurie Butler Lawrence
Reg. No. 46,593

Fish & Richardson P.C.
225 Franklin Street
Boston, MA 02110-2804
Telephone: (617) 542-5070
Facsimile: (617) 542-8906

Exhibit A



results of **BLAST**

BLASTP 2.2.7 [Jan-02-2004]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1075243340-3602-98206073622.BLASTQ3

Query=

(209 letters)

Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF

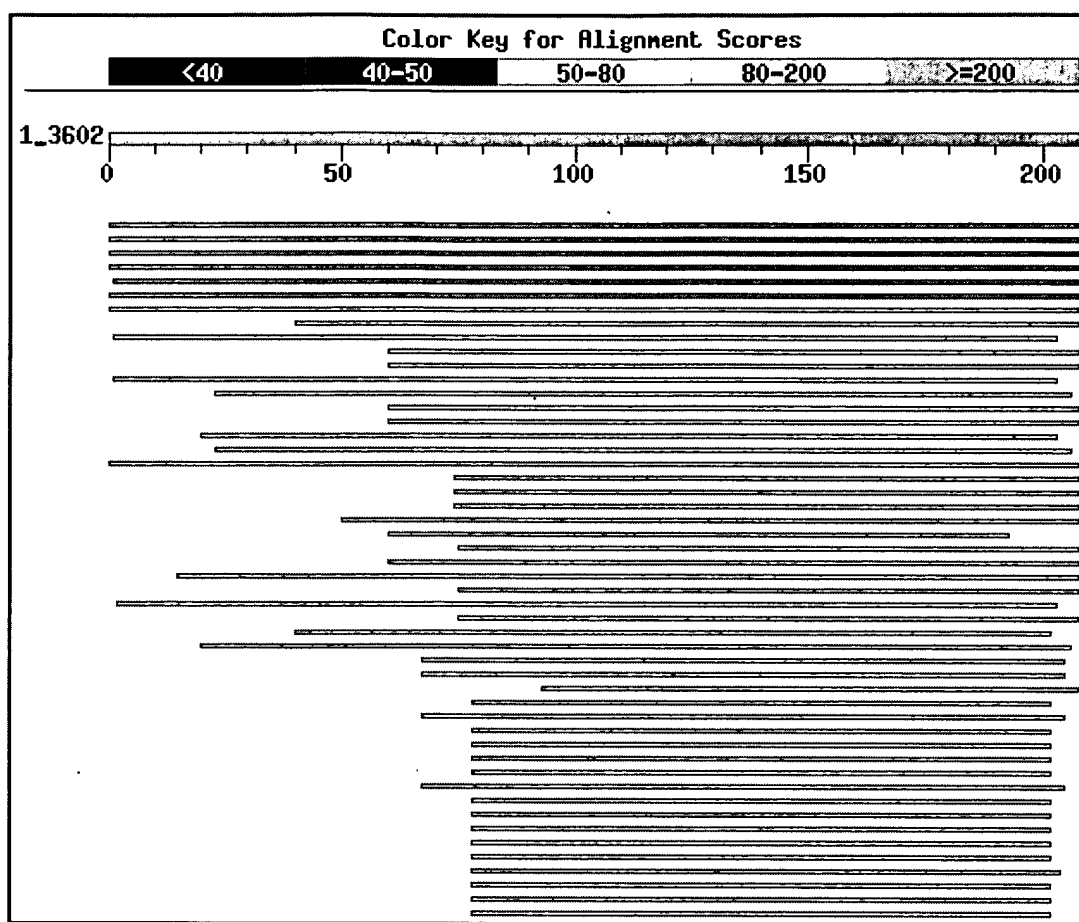
1,612,710 sequences; 530,365,172 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)
















[Taxonomy reports](#)

Distribution of 100 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Related Structures

Sequences producing significant alignments:			Score (bits)	E Value	
gi 9910158 ref NP_064385.1	C-type (calcium dependent, carb...	276	2e-73		
gi 37181558 gb AAQ88590.1	CLECSF11 [Homo sapiens]	224	8e-58		
gi 18466806 ref NP_569708.1	C-type (calcium dependent, car...	223	2e-57		
gi 7677472 gb AAF67178.1	dectin-2 beta isoform [Mus musculus]	220	1e-56		
gi 38085039 ref XP_355810.1	similar to dendritic cell immu...	209	3e-53		
gi 31978955 gb AAP58453.1	dendritic cell immuno-activating...	202	3e-51		
gi 7677475 gb AAF67179.1	dectin-2 gamma isoform [Mus muscu...	198	5e-50		
gi 17225339 gb AAL37359.1	dendritic lectin b isoform [Homo...	191	8e-48		
gi 31542313 ref NP_525126.2	C-type lectin, superfamily mem...	160	1e-38		
gi 25392205 pir JC7608	type II lectin-like immunoreceptor ...	160	1e-38		
gi 7705338 ref NP_057268.1	C-type lectin, superfamily memb...	160	2e-38		
gi 17226268 gb AAL37713.1	C-type lectin-like receptor CLEC...	159	3e-38		
gi 26354554 dbj BAC40905.1	unnamed protein product [Mus mu...	159	3e-38		
gi 8489015 gb AAF75560.1	HDCGC13P [Homo sapiens]	158	5e-38		
gi 37577115 ref NP_919429.1	C-type lectin, superfamily mem...	157	8e-38		
gi 34858421 ref XP_342754.1	similar to C-type lectin [Ratt...	157	1e-37		
gi 6754728 ref NP_034949.1	C-type lectin, superfamily memb...	156	2e-37		
gi 11493654 gb AAG35593.1	C-type lectin DDB27 short form [...	155	5e-37		

gi 13386214 ref NP_081494.1	RIKEN cDNA 1810046I24; DCAR al...	155	6e-37	L
gi 37577119 ref NP_919432.1	C-type lectin, superfamily mem...	154	7e-37	L
gi 37577117 ref NP_919430.1	C-type lectin, superfamily mem...	152	4e-36	L
gi 13879298 gb AAH06623.1	Clecsf6 protein [Mus musculus]	151	6e-36	L
gi 18028293 gb AAL56016.1	Fc-epsilon receptor III [Homo sa...	148	7e-35	L
gi 23397421 ref NP_694877.1	RIKEN cDNA 3110037K17 [Mus mus...	147	1e-34	L
gi 6753442 ref NP_036129.1	C-type (calcium dependent, carb...	147	1e-34	L
gi 25050261 ref XP_194289.1	similar to C-type lectin, supe...	142	3e-33	L
gi 26387827 dbj BAC25626.1	unnamed protein product [Mus mu...	142	4e-33	L
gi 7657333 ref NP_055173.1	C-type lectin, superfamily memb...	140	2e-32	L
gi 34858417 ref XP_342753.1	similar to RIKEN cDNA 3110037K...	140	2e-32	L
gi 34858419 ref XP_232393.2	similar to dendritic cell immu...	137	1e-31	L
gi 9910162 ref NP_064332.1	C-type lectin, superfamily memb...	129	4e-29	L
gi 25392184 pir JC7595	scavenger receptor with C-type lect...	96	5e-19	L
gi 38174510 gb AAH60789.1	Collectin sub-family member 12, ...	96	5e-19	L
gi 34858415 ref XP_342752.1	similar to C-type (calcium dep...	96	6e-19	L
gi 27356791 gb AAL89528.1	putative CD209L1 protein [Hyloba...	95	8e-19	
gi 18641360 ref NP_569057.1	collectin sub-family member 12...	95	8e-19	L
gi 27356800 gb AAL89529.1	putative CD209L1 protein [Hyloba...	95	9e-19	
gi 27356809 gb AAL89530.1	putative CD209L1 protein [Hyloba...	95	1e-18	
gi 12084795 gb AAG13815.2	probable mannose binding C-type ...	94	2e-18	L
gi 20149606 ref NP_055072.2	CD209 antigen-like; putative t...	93	3e-18	L
gi 19584340 emb CAD28466.1	hypothetical protein [Homo sapi...	92	4e-18	L
gi 27356856 gb AAL89536.1	putative CD209L1 protein [Pan tr...	92	6e-18	
gi 15383614 gb AAK91863.1	sDC-SIGN2 type I isoform [Homo s...	91	9e-18	L
gi 18157520 dbj BAB83835.1	supported by GENSCAN and partia...	91	9e-18	
gi 27356845 gb AAL89534.1	putative CD209L1 protein [Gorill...	91	9e-18	
gi 34870124 ref XP_344065.1	similar to SIGNR3 [Rattus norv...	91	1e-17	L
gi 27356883 gb AAL89539.1	putative CD209 protein [Hylobate...	91	2e-17	
gi 27356854 gb AAL89535.1	putative CD209L1 protein [Pan tr...	91	2e-17	
gi 12084797 gb AAG13848.2	probable mannose binding C-type ...	90	2e-17	L
gi 27356874 gb AAL89538.1	putative CD209 protein [Hylobate...	89	4e-17	
gi 15383618 gb AAK91865.1	sDC-SIGN2 type III isoform [Homo...	89	4e-17	L
gi 27356910 gb AAL89542.1	putative CD209 protein [Pongo py...	89	5e-17	
gi 27356901 gb AAL89541.1	putative CD209 protein [Pongo py...	89	6e-17	
gi 6680734 ref NP_031519.1	asialoglycoprotein receptor 2 [...	89	7e-17	L
gi 27356928 gb AAL89544.1	putative CD209 protein [Pan trog...	89	7e-17	
gi 34877879 ref XP_341575.1	similar to collectin placenta ...	88	8e-17	L
gi 27356892 gb AAL89540.1	putative CD209 protein [Hylobate...	88	9e-17	
gi 16118455 gb AAL14428.1	dendritic cell-specific ICAM-3 g...	88	1e-16	
gi 16118475 gb AAL14438.1	dendritic cell-specific ICAM-3 g...	88	1e-16	
gi 18652791 gb AAK74185.1	type II membrane protein CD209 [...	88	1e-16	
gi 15420784 gb AAK97459.1	dendritic cell-specific ICAM-3 g...	88	1e-16	
gi 15420782 gb AAK97458.1	dendritic cell-specific ICAM-3 g...	88	1e-16	
gi 37779180 gb AAP03436.1	dendritic cell-specific ICAM-3 g...	87	1e-16	
gi 23498707 emb CAD28398.1	putative mannose-binding C-type...	87	1e-16	
gi 10863957 ref NP_066978.1	CD209 antigen; dendritic cell-...	87	1e-16	L
gi 27356865 gb AAL89537.1	putative CD209 protein [Papio ha...	87	1e-16	
gi 27356919 gb AAL89543.1	putative CD209 protein [Gorilla ...	87	1e-16	
gi 15281089 gb AAK91854.1	mDC-SIGN1B type I isoform [Homo ...	87	2e-16	L
gi 27356930 gb AAL89545.1	putative CD209 protein [Pan trog...	87	2e-16	

gi 4502253 ref NP_001172.1	asialoglycoprotein receptor 2 i...	87	2e-16	L
gi 15281081 gb AAK91850.1	sDC-SIGN1A type I isoform [Homo ...	87	3e-16	L
gi 33328316 gb AAQ09608.1	HBxAg-binding protein [Homo sapi...	87	3e-16	L
gi 34870060 ref XP_341024.1	similar to CD209 antigen; dend...	87	3e-16	L
gi 15281077 gb AAK91848.1	mDC-SIGN1A type III isoform [Hom...	86	3e-16	L
gi 15281091 gb AAK91855.1	sDC-SIGN1B type I isoform [Homo ...	86	4e-16	L
gi 23498708 emb CAD28399.1	putative mannose-binding C-type...	86	4e-16	
gi 15281083 gb AAK91851.1	sDC-SIGN1A TYPE II isoform [Homo...	86	4e-16	L
gi 22651471 gb AAL71882.1	C-type lectin CD209L2 [Macaca mu...	86	5e-16	
gi 18426877 ref NP_550436.1	asialoglycoprotein receptor 2 ...	86	6e-16	L
gi 8392926 ref NP_058885.1	asialoglycoprotein receptor 2; ...	86	6e-16	L
gi 18426875 ref NP_550435.1	asialoglycoprotein receptor 2 ...	85	7e-16	L
gi 33667103 ref NP_878910.1	C-type lectin, superfamily mem...	85	7e-16	L
gi 5453684 ref NP_006335.1	C-type (calcium dependent, carb...	85	7e-16	L
gi 206649 gb AAA42038.1	asialoglycoprotein receptor (RHL2)	85	7e-16	L
gi 16758588 ref NP_446205.1	C-type lectin, superfamily mem...	85	8e-16	L
gi 18777736 ref NP_570974.1	CD209d antigen [Mus musculus] ...	85	9e-16	L
gi 15281093 gb AAK91856.1	sDC-SIGN1B type II isoform [Homo...	85	9e-16	L
gi 126136 sp P08290 LECI_RAT	Asialoglycoprotein receptor R2...	85	1e-15	
gi 15928688 gb AAH14811.1	Macrophage galactose N-acetyl-ga...	84	1e-15	L
gi 17017253 gb AAL33584.1	SIGNR3 [Mus musculus]	84	1e-15	L
gi 6754688 ref NP_034926.1	macrophage galactose N-acetyl-g...	84	1e-15	L
gi 26335321 dbj BAC31361.1	unnamed protein product [Mus mu...	84	1e-15	
gi 21901969 dbj BAC05523.1	collectin placenta 1 [Mus muscu...	84	1e-15	L
gi 15281085 gb AAK91852.1	sDC-SIGN1A type III isoform [Hom...	84	2e-15	L
gi 18158893 pdb 1K9J A	Chain A, Complex Of Dc-Signr And Glc...	83	3e-15	S
gi 18485494 ref NP_569716.1	collectin sub-family member 12...	83	4e-15	L
gi 34870118 ref XP_221808.2	similar to DC-SIGN [Rattus nor...	82	4e-15	L

Alignments

Get selected sequences

Select all

Deselect all

☐ >gi|9910158|ref|NP_064385.1| **L** C-type (calcium dependent, carbohydrate recognit:
superfamily member 10 [Mus musculus]
gi|7677469|gb|AAF67177.1| **L** dectin-2 alpha isoform [Mus musculus]
gi|18606438|gb|AAH23008.1| **L** C-type (calcium dependent, carbohydrate recognition
superfamily member 10 [Mus musculus]
Length = 209

Score = 276 bits (706), Expect = 2e-73

Identities = 144/211 (68%), Positives = 162/211 (76%), Gaps = 4/211 (1%)

Query: 1 MMQEQQPQSTKRGWLSLRLWSVAGISIALLSACFIVSCVVTYHFTYGETGKRLSELHSY 60

M+QE+Q Q K +LRLWS A IS+ LLS CFI SCVVTY F + +RL ELH+Y

Sbjct: 1 MVQERQSQG--KGVCWTLRLWSAAVISMILLSTCFIASCVVTYQFIMDQPSRRLYELHTY 58

Query: 61 HSSLTCFSEGTKVPA--WGCPASWKSFGSSCYFISSEEKVWSKSEQNCVEMGAHLVVFN 118

HSSLTCFSEGT V WGCCP WKSFGSSCY IS++E WS SEQNCV+MGAHLVV N
 Sbjct: 59 HSSLTCFSEGTMVSEKMWGCCPNHWKSFGSSCYLISTKENFWSTSEQNCVQMGAHLVVIN 118
 Query: 119 TEAEQNFIVQQLNESFSYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSAEQCAS 178
 TEAEQNF I QQLNES SYFLGLSDPQGN WQWID TP+ +NVRFWH EPN E+C S
 Sbjct: 119 TEAEQNFITQQLNESLSYFLGLSDPQNGKWQWIDDTFFSQNVRFWHPHEPNLPEERCVS 178
 Query: 179 IVFWKPTGWGWNDVICETRRNSICEMNKIYL 209
 IV+W P+ GWWNDV C+++ NSICEM KIYL
 Sbjct: 179 IVYWNPSKWGWNDVFCDSKHNSICEMKKIYL 209

☐ >gi|37181558|gb|AAQ88590.1| CLECSF11 [Homo sapiens]
 Length = 213

Score = 224 bits (571), Expect = 8e-58
 Identities = 116/213 (54%), Positives = 146/213 (68%), Gaps = 4/213 (1%)

Query: 1 MMQEQQPQSTEK-RGWLSLRLWSVAGISIALLSACFIVSCVVTYHFTYGETGKRLSEL-- 57
 M+ E++PQ EK W L++WS+A +SI LLS CF VS VV ++F Y +T KRLS+L
 Sbjct: 1 MVPEEPPQDREKGLWWFQLKVWSMAVVSILLLSVCFTVSSVVPNFMYSKTVKRLSKLRE 60
 Query: 58 -HSYHSSLTCFSEGTKVPAWGCCPASWKSFGSSCYFISSEKVKWSKSEQNCVEMGAHLVV 116
 YHSSLTC EG + W CCP W SF SSCYFIS+ + W+KS++NC MGA LVV
 Sbjct: 61 YQQYHSSLTCVMEGKDIEDWSCCPTPWTSFQSSCYFISTGMQSWTKSQKNCSVMGADLVV 120
 Query: 117 FNTEAEQNFIVQQLNESFSYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSAEQC 176
 NT EQ+FI+Q L + SYFLGLSDP G +WQW+D+TPY +NV FWH GEPN+ E+C
 Sbjct: 121 INTREEQDFIIQNLKRNSYFLGLSDPGRRHWQWVDQTPYNENVTFWHSGEPNNLDERC 180
 Query: 177 ASIVFWKPTGWGWNDVICETRRNSICEMNKIYL 209
 A I F GWWND+ C + SIC+M KIY+
 Sbjct: 181 AIINFRSSEEWGWNDIHCHVPQKSICKMKKIYI 213

☐ >gi|18466806|ref|NP_569708.1| ☒ C-type (calcium dependent, carbohydrate-recognition domain) lectin superfamily member 11; dendritic cell lectin b; blood dendritic cell antigen 2 protein; C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 7 [Homo sapiens]

gi|17224598|gb|AAL37036.1| ☒ blood dendritic cell antigen 2 protein [Homo sapiens]
 gi|17225337|gb|AAL37358.1| ☒ dendritic lectin [Homo sapiens]
 Length = 213

Score = 223 bits (568), Expect = 2e-57
 Identities = 115/213 (53%), Positives = 145/213 (68%), Gaps = 4/213 (1%)

Query: 1 MMQEQQPQSTEK-RGWLSLRLWSVAGISIALLSACFIVSCVVTYHFTYGETGKRLSEL-- 57
 M+ E++PQ EK W L++WS+A +SI LLS CF VS VV ++F Y +T KRLS+L
 Sbjct: 1 MVPEEPPQDREKGLWWFQLKVWSMAVVSILLLSVCFTVSSVVPNFMYSKTVKRLSKLRE 60
 Query: 58 -HSYHSSLTCFSEGTKVPAWGCCPASWKSFGSSCYFISSEKVKWSKSEQNCVEMGAHLVV 116
 YH SLTC EG + W CCP W SF SSCYFIS+ + W+KS++NC MGA LVV
 Sbjct: 61 YQQYHPSLTCVMEGKDIEDWSCCPTPWTSFQSSCYFISTGMQSWTKSQKNCSVMGADLVV 120
 Query: 117 FNTEAEQNFIVQQLNESFSYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSAEQC 176
 NT EQ+FI+Q L + SYFLGLSDP G +WQW+D+TPY +NV FWH GEPN+ E+C

Sbjct: 121 INTREEQDFIIQNLKRNSYFLGLSDPGGRRHWQWVDQTPYNENVTFWHSGEPPNNLDERC 180

Query: 177 ASIVFWKPTGWGWNDVICETRRNSICEMNKIYL 209
A I F WGWND+ C + SIC+M KIY+

Sbjct: 181 AIINFRSSEEWGWNDIHCHVPQKSICKMKKIYI 213

☐ >gi|7677472|gb|AAF67178.1| ☒ dectin-2 beta isoform [Mus musculus]
Length = 175

Score = 220 bits (560), Expect = 1e-56

Identities = 122/209 (58%), Positives = 137/209 (65%), Gaps = 34/209 (16%)

Query: 1 MMQEQQPQSTEKRGWLSLRLWSVAGISIALLSACFIVSCVVTYHFTYGETGKRLSELHSY 60
M+QE+Q Q K +LRLWS A IS+ LLS CFI SCV

Sbjct: 1 MVQERQSQG--KGVCWTLRLWSAAVISMLLLSTCFIASCVEK----- 40

Query: 61 HSSLTCFSEGTKVPAWGCCPASWKSFGSSCYFISSEKVVSKSEQNCVEMGAHLVVFNTE 120
WGCCP WKSFGSSCY IS++E WS SEQNCV+MGHLVV NTE

Sbjct: 41 -----MWGCCPNHWKSFGSSCYLISTKENFWSTSEQNCVQMGHLVVINTE 86

Query: 121 AEQNFIVQQLNESFSYFLGLSDPQGNMNWQWIDKTPYEKNVRFWHLGEPNHSAEQCASIV 180
AEQNFI QQLNES SYFLGLSDPQGN WQWID TP+ +NVRFWH EPN E+C SIV

Sbjct: 87 AEQNFITQQLNESLSYFLGLSDPQNGKWQWIDTTPFSQNVRFWHPHEPNLPEERCVSIV 146

Query: 181 FWKPTGWGWNDVICETRRNSICEMNKIYL 209
+W P+ WGWNDV C+++ NSICEM KIYL

Sbjct: 147 YWNPSKWGWNDVFCDSKHNSICEMMKKIYL 175

☐ >gi|38085039|ref|XP_355810.1| ☒ similar to dendritic cell immuno-activating receptor
DCAR alpha isoform [Mus musculus]
Length = 208

Score = 209 bits (532), Expect = 3e-53

Identities = 109/211 (51%), Positives = 141/211 (66%), Gaps = 6/211 (2%)

Query: 2 MQEQQPQSTEKRGWLSLRLWSVAGISIALLSACFIVSCVVTYHFTYGETGKRLSELHSYH 61
M +++P + W SLRLW A ISI LLS CFI SCVVTY + +RLSELH+YH

Sbjct: 1 MMQERPAQGQVVCW-SLRLWMAALISILLSTCFIASCVVTYQLMMNKPNNRLSELHTYH 59

Query: 62 SSLTCFSEGTKVP--AWGCCPASWKSFGSSCYFISSEKVV-SKSEQNCVEMGAHLVVFN 118
S+L CFSEGT V W CCP WK FGS CYF S++ + +KSE+ C GAHLVV +

Sbjct: 60 SNLICFSEGTTVSEKVVSCCPKDWKPFGSYCYFTSTDSRASQNKSEKCSLRGAHLVVIH 119

Query: 119 TEAEQNFIVQQLNESFSYFLGLSDPQGNMNWQWIDKTPYEKNVRFWHLGEPNHSAEQCAS 178
++ EQ+FI + L+ + YF+GLSD GN+ W+WID+TPY FWH GEPN+ E+C

Sbjct: 120 SQEEQDFITRMLDTAAGYFIGLSD-VGNSQWRWIDQTPYNDRATFWHKGEPNNDYEKCV- 177

Query: 179 IVFWKPTGWGWNDVICETRRNSICEMNKIYL 209
I+ ++ T WGWND+ C NS+C+M KIYL

Sbjct: 178 ILNYRKTMWGWNDIDCSDEENSVCQMCKKIYL 208

☐ >gi|31978955|gb|AAP58453.1| dendritic cell immuno-activating receptor alpha isoform [Mus musculus]

Length = 209



Score = 202 bits (514), Expect = 3e-51
 Identities = 110/213 (51%), Positives = 143/213 (67%), Gaps = 8/213 (3%)

Query: 1 MMQEQQPQSTTEKRGWLSLRLWSVAGISIALLSACFIVSCVVITYHFTYGETGKRLSELHSY 60
 M+QE+Q Q + W SLRLWS A ISI LLS CFI SCVVITY F+ + +RLSEL Y
 Sbjct: 1 MVQERQLQG-KAVSW-SLRLWSAAVISILLSTCFIASCVVITYQFSMDKPNRRLSELDRY 58

Query: 61 HSSLTCFSEGTKVP--AWGCCPASWKSFGSSCYFISS--EEKVWSKSEQNCVEMGAHLVV 116
 HS LTCFSEG V W CCP WK FGS CY + + W+KSE+NC MGAHLVV
 Sbjct: 59 HS-LTCFSEG NMVSDK VWSGCCPKDWKLF GSHCYLVPTVFSSASWNKSEENC SRMGAHLVV 117

Query: 117 FNTEAEQNFI VQQLNESFSYFLGLSDPQGN NNWQWIDKTPYEKNVRFWHLGEPNHSAEQC 176
 +++ EQ+FI L+ +YF+GL D G+ WQW+D+TPYE++V FWH GEP+ E+C
 Sbjct: 118 IHSQEEQDFITGILDIHAAAYFIGLWD-TGHRQWQWVDQTPYEESVTFWHNGEPSSDNEKC 176

Query: 177 ASIVFWKPTGWGWNDVICETRRNSICEMNKIYL 209
 ++ + + GWGND+ C ++ S+C+M KI L
 Sbjct: 177 VTVYYRRNIGGWNDISCNLQKQSVCMKKINL 209

 >gi|7677475|gb|AAF67179.1|  dectin-2 gamma isoform [Mus musculus]
 Length = 168



Score = 198 bits (504), Expect = 5e-50
 Identities = 117/211 (55%), Positives = 132/211 (62%), Gaps = 45/211 (21%)

Query: 1 MMQEQQPQSTTEKRGWLSLRLWSVAGISIALLSACFIVSCVVITYHFTYGETGKRLSELHSY 60
 M+QE+Q Q K +LRLWS A IS+ LLS CFI SCVVITY F + +RL ELH+Y
 Sbjct: 1 MVQERQSQG--KGVCWTLRLWSAAVISMLLLSTCFIASCVVITYQFIMDQPSRRRLYLHTY 58

Query: 61 HSSLTCFSEGTKVPA--WGCCPASWKSFGSSCYFISSEEEKVWSKSEQNCVEMGAHLVVFN 118
 HSSLTCFSEG T V WGCCP WKSFGSSCY IS++E WS SEQNCV+MGAHLVV N
 Sbjct: 59 HSSLTCFSEG TMVSEK MWGCCPNHWKSFGSSCYLISTKENFWSTSEQNCVQMGAHLVVIN 118

Query: 119 TEAEQNFI VQQLNESFSYFLGLSDPQGN NNWQWIDKTPYEKNVRFWHLGEPNHSAEQCAS 178
 TEAEQNFI QQLNES SYFLGLS+P
 Sbjct: 119 TEAEQNFI TQQLNESLSYFLGLSNP----- 143

Query: 179 IVFWKPTGWGWNDVICETRRNSICEMNKIYL 209
 + GWGNDV C+++ NSICEM KIYL
 Sbjct: 144 -----SKWGWNDVFCDSKHNSICEMKKIYL 168

 >gi|17225339|gb|AAL37359.1|  dendritic lectin b isoform [Homo sapiens]
 Length = 182

Score = 191 bits (484), Expect = 8e-48
 Identities = 94/172 (54%), Positives = 117/172 (68%), Gaps = 3/172 (1%)

Query: 41 VTYHFTYGETGKRLSEL---HSYHSSLTCFSEGTKVPAWGCCPASWKSFGSSCYFISSEE 97
 V ++F Y +T KRLS+L YH SLTC EG + W CCP W SF SSCYFIS+
 Sbjct: 11 VPHNFMYSKTVKRLSKLREYQQYHPSLTCVMEGKDIEDWSCCPTPWTSTFQSSCYFISTGM 70

Query: 98 KVWSKSEQNCVEMGAHLVVFNTEAEQNFI VQQLNESFSYFLGLSDPQGN NNWQWIDKTPY 157
 + W+KS++NC MGA LVV NT EQ+FI+Q L + SYFLGLSDP G +WQW+D+TPY

Sbjct: 71 QSWTKSQKNCSVMGADLVVINTREEQDFIIQNLKRNSSYFLGLSDPGGRRHWQWVDQTPY 130

Query: 158 EKNVRFWHLGEPNHSAEQCASIVFWKPTGWGWNDVICETRRNSICEMNKIYL 209
+NV FWH GEPN+ E+CA I F WGWN+ C + SIC+M KIY+

Sbjct: 131 NENVTFWHSGEPNLDERCAIINFRSSEEWGWNDIHCHVPQKSICKMKKIYI 182

[gi|31542313|ref|NP_525126.2|](#) [C-type lectin, superfamily member 8; C-type lectin](#)
[Homo sapiens]

[gi|21595255|gb|AAH32313.1|](#) [C-type lectin, superfamily member 8 \[Homo sapiens\]](#)
Length = 215

Score = 160 bits (406), Expect = 1e-38

Identities = 84/210 (40%), Positives = 126/210 (60%), Gaps = 8/210 (3%)

Query: 2 MQEQQPQSTTEKRGWLSLRLWSV-AGISIALLSACFIVSCVVTYH-FTYGETGKRLSELHS 59
M ++PQS + G + SV A + I LLS CFI SC+VT+H F+ + G + +L

Sbjct: 1 MGLEKPPQSKLEGGMHPQLIPSVIAVVFILLLSVCFIASCLVTHHNFSRCKRGTGVHKL- 59

Query: 60 YHSSLTCFSEGTKVPA-----WGCCPASWKSFGSSCYFISSEKQVWSKSEQNCVEMGAHL 114
+H+ L C E +++ + W CCP W++F S+CYF ++ K W++SE+NC MGAHL

Sbjct: 60 HHAKLKCIKEKSELKSAEGSTWNCCPIDWRAFQSNCFPLTDNKTWAESERNCSGMGAHL 119

Query: 115 VVFNTAEQNFIVQQLNESFSYFLGLSDPQGNWQWIDKTPYEKNVRFWHLGEPNHSAE 174
+ +TEAEQNF+Q L+ SYFLGL D W+W+D+TP+ FWH EP++S

Sbjct: 120 MTISTAEQNFIIQFLDRRLSYFLGLRDENAKGQWRWVDQTPFNPRRVFWHKNEPDNSQG 179

Query: 175 QCASIVFWKPTGWGWNDVICETRRNSICEM 204
+ ++ + W WNDV C + IC++

Sbjct: 180 ENCIVLVYNQDKAWNDVPCNFEASRICKI 209

[gi|25392205|pir|JC7608](#) type II lectin-like immunoreceptor - human
[gi|6502535|gb|AAF14348.1|](#) [C-type lectin superfamily 6 \[Homo sapiens\]](#)
Length = 237

Score = 160 bits (405), Expect = 1e-38

Identities = 77/152 (50%), Positives = 102/152 (67%), Gaps = 3/152 (1%)

Query: 61 HSSLTCFSEGTKV--PAWGCPASWKSFGSSCYFISSEKQVWSKSEQNCVEMGAHLVFN 118
H++L C + V AW CCP +WKSF S+CYFIS+E W SE++C M AHL+V N

Sbjct: 86 HTTLECVKKNMPVEETAWSCCPKNWKSFSNNCYFISTESASWQDSEKDCARMEAHLLVIN 145


Query: 119 TEAEQNFIVQQLNESFSYFLGLSDPQGNWQWIDKTPYEKNVRFWHLGEPNHSAEQCAS 178
T+ EQ+FI Q L E +YF+GLSDP+G +WQW+D+TPY ++ FWH EP+ E+C

Sbjct: 146 TQEEQDFIFQNLQEESAYFVGLSDPEGQRHWQWVDQTPYNESSTFWHPREPSDPNERCVV 205

Query: 179 IVFWK-PTGWGWNDVICETRRNSICEMNKIYL 209
+ F K P WGWN+ C + S+CEM KI+L

Sbjct: 206 LNFRKSPKRWGWNDVNCLGPQRSVCEMMKIHL 237

[gi|7705338|ref|NP_057268.1|](#) [C-type lectin, superfamily member 6 isoform 1; de](#)
immunoreceptor; C-type lectin; lectin-like
immunoreceptor [Homo sapiens]

gi|5823974|emb|CAB54001.1|  dendritic cell immunoreceptor [Homo sapiens]
Length = 237

Score = 160 bits (404), Expect = 2e-38

Identities = 77/152 (50%), Positives = 102/152 (67%), Gaps = 3/152 (1%)

Query: 61 HSSLTCFSEGTKV--PAWGCCPASWKSFGSSCYFISSEEEKVWSKSEQNCVEMGAHLVVFN 118
H++L C + V AW CCP +WKSF S+CYFIS+E W SE++C M AHL+V N

Sbjct: 86 HTTLECVKKNMPVEETAWSCCPKNWKSFSNCFISTESASWQDSEKDCARMEAHLLVIN 145


Query: 119 TEAEQNFIQQQLNESFSYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSAEQCAS 178
T+ EQ+FI Q L E +YF+GLSDP+G +WQW+D+TPY ++ FWH EP+ E+C


Sbjct: 146 TQEEQDFIFQNLQEESAYFVGLSDPEGQRHWQWVDQTPYNESSTFWHPREPSDPNERCVV 205

Query: 179 IVFWK-PTGWGWNDVICETRRNSICEMNKIYL 209

+ F K P WGWNDV C + S+CEM KI+L

Sbjct: 206 LNFRKSPKRWGWNDVNCLGPQRSVCEMMKIHL 237

>gi|17226268|gb|AAL37713.1|  C-type lectin-like receptor CLEC-6 [Homo sapiens]

gi|31321980|gb|AAM75389.1|  C-type lectin-like receptor 6 [Homo sapiens]
Length = 215

Score = 159 bits (402), Expect = 3e-38

Identities = 83/210 (39%), Positives = 125/210 (59%), Gaps = 8/210 (3%)

Query: 2 MQEQQPQSTEKRWLSLRLWSV-AGISIALLSACFIVSCVVTYH-FTYGETGKRLSELHS 59
M ++PQS + G + SV A + I LL CFI SC+VT+H F+ + G + +L

Sbjct: 1 MGLEKPKSKLEGGMHPQLIPSVIAVVFILLGLVCFIASCLVTHHNFSRCKRGTGVHKL- 59

Query: 60 YHSSLTCFSEGTKVPA-----WGCCPASWKSFGSSCYFISSEEEKVWSKSEQNCVEMGAHL 114
+H+ L C E +++ + W CCP W++F S+CYF ++ K W++SE+NC MGAHL

Sbjct: 60 HHAKLKCIKEKSELKSAEGSTWNCCPIDWRAFQSNCFPLTDNKTWAESERNCSGGMGAHL 119

Query: 115 VVFNTAEQNFIVQQQLNESFSYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSAE 174
+ +TEAEQNFI+Q L+ SYFLGL D W+W+D+TP+ FWH EP++S

Sbjct: 120 MTISTAEQNFIIQFLDRRLSYFLGLRDENAKGQWRWVDQTPFNPRRVFVHKNEPDNSQG 179

Query: 175 QCASIVFWKPTGWGWNDVICETRRNSICEM 204

+ ++ + W WNDV C + IC++

Sbjct: 180 ENCIVLVYNQDKAWNDVPCNFEASRICKI 209

>gi|26354554|dbj|BAC40905.1| unnamed protein product [Mus musculus]
Length = 219

Score = 159 bits (402), Expect = 3e-38

Identities = 81/188 (43%), Positives = 113/188 (60%), Gaps = 4/188 (2%)

Query: 24 AGISIALLSACFIVSCVVTYHFTYGETGKRLSELHSYHSSLTCFSEGTKVPA---WGCC 79
A +SI+ LSACFI +C+VT+H+ T + +L YH+ +TC EG + A W CC



Sbjct: 24 AVVSISIFLSACFISTCLVTHHYFLRWTRGSVVKLSDYHTRVTCIREGPQPGATGGTWTCC 83

Query: 80 PASWKSFGSSCYFISSEEEKVWSKSEQNCVEMGAHLVVFNTAEQNFIVQQQLNESFSYFLG 139
P SW++F S+CYF ++ + W +SE+NC M +HLV NTEAEQNFI+ Q L++ FSYFLG

Sbjct: 84 PVSWRAFQSNCFPLNDNQTHWESERNCSGMSHSLVTINTEAEQNFVTQLLDKRFSYFLG 143

Query: 140 LSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSAEQCASIVFWKPTGWGWNDVICETRRN 199
 L+D WQW+DKTP+ + FW GE N E+ ++ W WND C
 Sbjct: 144 LADENVEGQWQWVDKTPFNPHTVFWKEGESNDFMEEDCVVLVHVHEKWVWVNDPCHFEVR 203

Query: 200 SICEMNKI 207
 IC++ I
 Sbjct: 204 RICKLPGI 211



 >gi|8489015|gb|AAF75560.1|  HDCGC13P [Homo sapiens]
 Length = 237

Score = 158 bits (400), Expect = 5e-38
 Identities = 76/152 (50%), Positives = 101/152 (66%), Gaps = 3/152 (1%)

Query: 61 HSSLTCFSEGTKV--PAWGCCPASWKSFGSSCYFISSEKVVWSKSEQNCVEMGAHLVVFN 118
 H++L C + V AW CCP +WKSF S+CYFIS+E W E++C M AHL+V N
 Sbjct: 86 HTTLECVKKNMPVEETAWSCCPKNWKSFSNCFISTESASWQDCEKDCARMEAHLLVIN 145

Query: 119 TEAEQNFIVQQNLNESFSYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSAEQCAS 178
 T+ EQ+FI Q L E +YF+GLSDP+G +WQW+D+TPY ++ FWH EP+ E+C
 Sbjct: 146 TQEEQDFIFQNLQEESAYFVGLSDPEGQRHWQWVDQTPYNESSTFWHPREPSDPNERCVV 205

Query: 179 IVFWK-PTGWGWNDVICETRRNSICEMNKIYL 209
 + F K P GWNDV C + S+CEM KI+L
 Sbjct: 206 LNFRKSPKRWGWNVDNCLGPQRSVCEMMKIHL 237



 >gi|37577115|ref|NP_919429.1|  C-type lectin, superfamily member 6 isoform 3; c
 immunoreceptor; C-type lectin; lectin-like
 immunoreceptor [Homo sapiens]
 Length = 197

Score = 157 bits (398), Expect = 8e-38
 Identities = 77/152 (50%), Positives = 102/152 (67%), Gaps = 3/152 (1%)

Query: 61 HSSLTCFSEGTKV--PAWGCCPASWKSFGSSCYFISSEKVVWSKSEQNCVEMGAHLVVFN 118
 H++L C + V AW CCP +WKSF S+CYFIS+E W SE++C M AHL+V N
 Sbjct: 46 HTTLECVKKNMPVEETAWSCCPKNWKSFSNCFISTESASWQDSEKDCARMEAHLLVIN 105

Query: 119 TEAEQNFIVQQNLNESFSYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSAEQCAS 178
 T+ EQ+FI Q L E +YF+GLSDP+G +WQW+D+TPY ++ FWH EP+ E+C
 Sbjct: 106 TQEEQDFIFQNLQEESAYFVGLSDPEGQRHWQWVDQTPYNESSTFWHPREPSDPNERCVV 165

Query: 179 IVFWK-PTGWGWNDVICETRRNSICEMNKIYL 209
 + F K P GWNDV C + S+CEM KI+L
 Sbjct: 166 LNFRKSPKRWGWNVDNCLGPQRSVCEMMKIHL 197

 >gi|34858421|ref|XP_342754.1|  similar to C-type lectin [Rattus norvegicus]
 Length = 226

Score = 157 bits (397), Expect = 1e-37
 Identities = 83/196 (42%), Positives = 114/196 (58%), Gaps = 13/196 (6%)




Query: 21 WSVAGISIALLSACFIVSCV-----VTYHFTYGETGKRLSELHSHSSLTCFSE--- 69

W A +SI+ LSACFI +C+ VT++F + G L + YH+ LTC E
 Sbjct: 21 WVCAVVSISFLSACFISTCLGKLLFLLTVTHYFLLWKRGSAI-KFSDYHTRLTCILEEPQ 79

Query: 70 -GTKVPAWGCCPASWKSFGSSCYFISSEKVVWSKSEQNCVEMGAHLVVFNTAEQNFIVQ 128
 G W CCP SW++F S+CYF ++ + W +SE+NC M +HLV NTEAEQ+F+ Q
 Sbjct: 80 PGATGGTWTCCPVSWRAFQSNCFPLNDNQTHESERNCSGMSSHLVTINTEAEQDFVTQ 139

Query: 129 QLNEFSYFLGLSDPQGNWQWIDKTPYEKNVRFWHLGEPNHSAEQCASIVFWKPTGWG 188
 L+E FSYFLGLS + WQW+DKTP+ NV FW +GEP E+ ++ + W
 Sbjct: 140 LLDEQFSYFLGLSYEKVEGQWQWVDKTPFPNPVFWKVGEPKDYMEEDCVVLVDQDKWV 199

Query: 189 WNDVICETRRNSICEM 204
 WND C IC++
 Sbjct: 200 WNDPCHFEMGRICKL 215

 >gi|6754728|ref|NP_034949.1|  C-type lectin, superfamily member 8; macrophage (C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 [Mus musculus]
 gi|4159801|gb|AAD05125.1|  C-type lectin [Mus musculus]
 Length = 219



Score = 156 bits (395), Expect = 2e-37
 Identities = 80/188 (42%), Positives = 111/188 (59%), Gaps = 4/188 (2%)

Query: 24 AGISIALLSACFIVSCVVTYHFTYGETGKRLSELHSYHSSLTCFSE----GTKVPAWGCC 79
 A +SI+ LSACFI +C+VT+H+ T + +L YH+ +TC E G W CC
 Sbjct: 24 AVVSISFLSACFISTCLVTHHYFLRWTRGSVVKLSYHTRVTCIREEPQPGATGGTWTCC 83

Query: 80 PASWKSFGSSCYFISSEKVVWSKSEQNCVEMGAHLVVFNTAEQNFIVQQLNESFSYFLG 139
 P SW++F S+CYF ++ + W +SE+NC M +HLV NTEAEQNF+ Q L++ FSYFLG
 Sbjct: 84 PVSWRAFQSNCFPLNDNQTHESERNCSGMSSHLVTINTEAEQNFVTQLLDKRFSYFLG 143

Query: 140 LSDPQGNWQWIDKTPYEKNVRFWHLGEPNHSAEQCASIVFWKPTGWGWNDVICETRRN 199
 L+D WQW+DKTP+ + FW GE N E+ ++ W WND C
 Sbjct: 144 LADENVEGQWQWVDKTPFPNPTVFWKESNDFMEEDCVVLVHVHEKVVWNDPCHFVR 203

Query: 200 SICEMNKI 207
 IC++ I
 Sbjct: 204 RICKLPGI 211

 >gi|11493654|gb|AAG35593.1|  C-type lectin DDB27 short form [Homo sapiens]
 Length = 204

Score = 155 bits (391), Expect = 5e-37
 Identities = 73/136 (53%), Positives = 95/136 (69%), Gaps = 1/136 (0%)

Query: 75 AWGCCPASWKSFGSSCYFISSEKVVWSKSEQNCVEMGAHLVVFNTAEQNFIVQQLNESF 134
 AW CCP +WKSF S+CYFIS+E W SE++C M AHL+V NT+ EQ+FI Q L E
 Sbjct: 69 AWSCCPKNWKSFSNNCFISTESASWQDSEKDCARMEAHLLVINTQEEQDFIFQNLQEE 128

Query: 135 SYFLGLSDPQGNWQWIDKTPYEKNVRFWHLGEPNHSAEQCASIVFWK-PTGWGWNDVI 193
 +YF+GLSDP+G +WQW+D+TPY ++ FWH EP+ E+C + F K P WGWNVDV
 Sbjct: 129 AYFVGLSDPEGQRHWQWVDQTPYNESSTFWHPREPSDPNERCVVLNFRKSPKRWGWNVDN 188

Query: 194 CETRRNSICEMNKIYL 209

C + S+CEM KI+L
 Sbjct: 189 CLGPQRSVCEMMKIHL 204

☐ >gi|13386214|ref|NP_081494.1| ☒ RIKEN cDNA 1810046I24; DCAR alpha; DCAR beta; d
 immunoactivating receptor [Mus musculus]
 gi|12841568|dbj|BAB25260.1| ☒ unnamed protein product [Mus musculus]
 gi|31978957|gb|AAP58454.1| ☒ dendritic cell immuno-activating receptor beta isofo
 isoform [Mus musculus]
 Length = 176

Score = 155 bits (391), Expect = 6e-37
 Identities = 90/211 (42%), Positives = 120/211 (56%), Gaps = 37/211 (17%)

Query: 1 MMQEQQPQSTKRGWLSLRLWSVAGISIALLSACFIVSCVVTYHFTYGETGKRLSELHSY 60
 M+QE+Q Q + W SLRLWS A ISI LLS CFI SCV
 Sbjct: 1 MVQERQLQG-KAVSW-SLRLWSAAVISILLSTCFIASCVDK----- 40
 Query: 61 HSSLTCFSEGTKVPAWGCCPASWKSFGSSCYFISS--EEKVWSKSEQNCVEMGAHLVVFN 118
 W CCP WK FGS CY + + W+KSE+NC MGAHLVV +
 Sbjct: 41 -----VWCCPKDWKLFGSHCYLVPTVFSSASWNKSEENC SRMGAHLVVIH 86
 Query: 119 TEAEQNFIVQQLNESFSYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSAEQCAS 178
 ++ EQ+FI L+ +YF+GL D G+ WQW+D+TPYE++V FWH GEP+ E+C +
 Sbjct: 87 SQEEQDFITGILDIHAAYFIGLWD-TGHRQWQWVDQTPYEESVTFWHNGEPSSDNEKCVT 145
 Query: 179 IVFWKPTGWGWNDVICETRNSICEMNKIYL 209
 + + + GWGWND+ C ++ S+C+M KI L
 Sbjct: 146 VYRRNIGGWNDISCNLKQKSVCMKKINL 176

☐ >gi|37577119|ref|NP_919432.1| ☒ C-type lectin, superfamily member 6 isoform 2; c
 immunoreceptor; C-type lectin; lectin-like
 immunoreceptor [Homo sapiens]
 Length = 204

Score = 154 bits (390), Expect = 7e-37
 Identities = 73/136 (53%), Positives = 95/136 (69%), Gaps = 1/136 (0%)

Query: 75 AWGCCPASWKSFGSSCYFISSEEEKVWSKSEQNCVEMGAHLVVFNTEAEQNFIVQQLNESF 134
 AW CCP +WKSF S+CYFIS+E W SE++C M AHL+V NT+ EQ+FI Q L E
 Sbjct: 69 AWCCPKNWKSFSNNCYFISTESASWQDSEKDCARMEHLLVINTQEEQDFIFQNLQEEES 128
 Query: 135 SYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSAEQCASIVFWK-PTGWGWNDVI 193
 +YF+GLSDP+G +WQW+D+TPY ++ FWH EP+ E+C + F K P GWWNDV
 Sbjct: 129 AYFVGLSDPEGQRHWQWVDQTPYNESSTFWHPRESDPNERC'VVLNFRKSPKRWGWNDVN 188
 Query: 194 CETRNSICEMNKIYL 209
 C + S+CEM KI+L
 Sbjct: 189 CLGPQRSVCEMMKIHL 204

☐ >gi|37577117|ref|NP_919430.1| ☒ C-type lectin, superfamily member 6 isoform 4; c
 immunoreceptor; C-type lectin; lectin-like
 immunoreceptor [Homo sapiens]

Length = 165

Score = 152 bits (383), Expect = 4e-36

Identities = 73/136 (53%), Positives = 95/136 (69%), Gaps = 1/136 (0%)

Query: 75 AWGCCPASWKSFGSSCYFISSEKVVWSKSEQNCVEMGAHLVVFNTAEQNFIVQQLNESF 134
 AW CCP +WKSF S+CYFIS+E W SE++C M AHL+V NT+ EQ+FI Q L E

Sbjct: 30 AWSCCPKNWKSFSNCFISTESASWQDSEKDCARMEAHLLVINTQEEQDFIFQNLQEEES 89


Query: 135 SYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSAEQCASIVFWK-PTGWGWNDVI 193
 +YF+GLSDP+G +WQW+D+TPY ++ FWH EP+ E+C + F K P WGWNDV

Sbjct: 90 AYFVGLSDPEGQRHWQWVDQTPYNESSTFWHPREPSDPNERCVVLNFRKSPKRWGWNDVN 149

Query: 194 CETRRNSICEMNKIYL 209

C + S+CEM KI+L

Sbjct: 150 CLGPQRSVCCEMMKIHL 165

 >gi|13879298|gb|AAH06623.1|  Clecsf6 protein [Mus musculus]

Length = 262

Score = 151 bits (382), Expect = 6e-36

Identities = 74/161 (45%), Positives = 102/161 (63%), Gaps = 5/161 (3%)

Query: 51 GKRLSELHSYHSSLTCFSEGTKVPAWGCCPASWKSFGSSCYFIS--SEEKVWSKSEQNCV 108
 G+R L S L + KV W CCP W+ FGS CY + S W+KSE+NC

Sbjct: 105 GQRALTLESIEIDLILAPEDKV--WSCCPKDWRLFGSHCYLVPTVSSASWNKSEENC 162



Query: 109 EMGAHLVVFNTAEQNFIVQQLNESFSYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGE 168
 MGAHLVV ++ EQ+FI L+ +YF+GL D G+ WQW+D+TPYE+++ FWH GE

Sbjct: 163 RMGAHLVVIQSQEEQDFITGILDTHAAYFIGLWD-TGHRQWQWVDQTPYEESITFWHNGE 221

Query: 169 PNHSAEQCASIVFWKPTGWGWNDVICETRRNSICEMNKIYL 209

P+ E+CA+I++ TGWGWND+ C ++ S+C+M KI L

Sbjct: 222 PSSGNEKCATIIRWKTGWGWNDISCSLKQKSVCQMCKINL 262

 >gi|18028293|gb|AAL56016.1|  Fc-epsilon receptor III [Homo sapiens]

Length = 230

Score = 148 bits (373), Expect = 7e-35

Identities = 70/137 (51%), Positives = 92/137 (67%), Gaps = 3/137 (2%)

Query: 61 HSSLTCFSEGTKV--PAWGCCPASWKSFGSSCYFISSEKVVWSKSEQNCVEMGAHLVVFN 118
 H++L C + V AW CCP +WKSF S+CYFIS+E W SE++C M AHL+V N

Sbjct: 86 HTTLECVKKNMPVEETAWSGCCPKNWKSFSNCFISTESASWQDSEKDCARMEAHLLVIN 145

Query: 119 TEAEQNFIVQQLNESFSYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSAEQCAS 178
 T+ EQ+FI Q L E +YF+GLSDP+G +WQW+D+TPY ++ FWH EP+ E+C

Sbjct: 146 TQEEQDFIFQNLQEEESAYFVGLSDPEGQRHWQWVDQTPYNESSTFWHPREPSDPNERCVV 205

Query: 179 IVFWK-PTGWGWNDVIC (194)

+ F K P WGWNDV C

Sbjct: 206 LNFRKSPKRWGWNDVNC 222

☐ >gi|23397421|ref|NP_694877.1| ☒ RIKEN cDNA 3110037K17 [Mus musculus]
 gi|22028415|gb|AAH34893.1| ☒ RIKEN cDNA 3110037K17 [Mus musculus]
 Length = 158

Score = 147 bits (372), Expect = 1e-34
 Identities = 70/135 (51%), Positives = 94/135 (69%), Gaps = 2/135 (1%)

Query: 76 WGCCPASWKSFGSSCYFISSE-EKVWSKSEQNCVEMGAHLVVFNTAEQNFIVQQLNESF 134
 W CCP WK FGS CYF S++ W++S++NC MGAHLVV +++ EQ+FI L+
 Sbjct: 25 WSCCPKDWKPFSGSYCYFTSTDLVASWNESEKENC FHMGAHLVVIHSQEEQDFITGILDTGT 84

Query: 135 SYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSAEQCASIVFWKPTGWGWNDVIC 194
 +YF+GLS+P G+ WQWID+TPY+ N FWH GEP+ EQC I + TGWGW+D+ C
 Sbjct: 85 AYFIGLSNP-GDQQWQWIDQTPYDDNTTFWHKGEPSDNEQCVIINHRQSTGWGWSDIPC 143

Query: 195 ETRRNSICEMNKIYL 209
 ++NSIC + KIIYL
 Sbjct: 144 SDKQNSICHVKKIYL 158

☐ >gi|6753442|ref|NP_036129.1| ☒ C-type (calcium dependent, carbohydrate recognition
 superfamily member 6; dendritic cell immunoreceptor [Mus
 musculus]
 gi|6018624|emb|CAB57870.1| ☒ dendritic cell immunoreceptor [Mus musculus]
 gi|20467064|gb|AAM22402.1| ☒ dendritic cell immunoreceptor [Mus musculus]
 gi|26339676|dbj|BAC33509.1| ☒ unnamed protein product [Mus musculus]
 Length = 238

Score = 147 bits (370), Expect = 1e-34
 Identities = 70/153 (45%), Positives = 99/153 (64%), Gaps = 5/153 (3%)

Query: 61 HSSLTCFSEGTKV--PAWGCCPASWKSFGSSCYFIS--SEEKVWSKSEQNCVEMGAHLVV 116
 H+ L C + + W CCP W+ FGS CY + S W+KSE+NC MGAHLVV
 Sbjct: 87 HNELNCTKSVSPMEDKVVSCCPKDWRLFGSHCYLVPTVSSSASWNKSEENCSRMGHLVV 146

Query: 117 FNTAEQNFIVQQLNESFSYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSAEQC 176
 ++ EQ+FI L+ +YF+GL D G+ WQW+D+TPYE+++ FWH GEP+ E+C
 Sbjct: 147 IQSQEEQDFITGILDTHAAYFIGLWD-TGHRQWQWVDQTPYEESITFWHNGEPSSGNEKC 205

Query: 177 ASIVFWKPTGWGWNDVICETRRNSICEMNKIYL 209
 A+I++ TGWGWND+ C ++ S+C+M KI L
 Sbjct: 206 ATIIYRWKTGWGWNDISCSLKQKSVQMKKINL 238

☐ >gi|25050261|ref|XP_194289.1| ☒ similar to C-type lectin, superfamily member 6
 cell immunoreceptor; C-type lectin; lectin-like
 immunoreceptor [Mus musculus]
 gi|29387373|gb|AAH49354.1| ☒ MGC56880 protein [Mus musculus]
 Length = 245

Score = 142 bits (359), Expect = 3e-33
 Identities = 74/198 (37%), Positives = 110/198 (55%), Gaps = 9/198 (4%)

Query: 16 LSLRLWSVAGISIALLSACFIVSCVVYHFTYGETGKRLSELHSYHSSLTCFSEGTKV-- 73
 L L LW I LL+ F V+ ++ + ++ + H+ L C + V

Sbjct: 53 LLLALW----IFFLLLAILFSVALIILFQMYSDLLLEEKYTLERLNHARLHCVKNHSSVED 108

Query: 74 PAWGCCPASWKSFGSSCYFISSEEKVVWSKSEQNCVEMGAHLVVFNTAEQNFIVQQLNES 133
W CCP +WK F S CYF S + WSKSE+ C GAHL+V ++ EQ+FI LN

Sbjct: 109 KVVSCCPKNWKPFDSHCYFTSRDTASWSKSEEKCSLRGAHLLVIQSQEEQDFITNTLNPR 168

Query: 134 FSYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSAEQCASIVFWKPT--GWGWND 191
+Y++GLSDP+G+ WQW+D+TPY++N WH EP+ + E C ++ + P GWGW+

Sbjct: 169 AAYYVGLSDPKGHGQWQWVDQTPYDQNSWHSDEPSGNTFCV-VLSYHPNVKGWGSV 227

Query: 192 VICETRRNSICEMNKIYL 209
C+ ICEM ++Y+

Sbjct: 228 APCDGDHRLICEMRQLYV 245

[gi|26387827|dbj|BAC25626.1|](#) [unnamed protein product \[Mus musculus\]](#)
Length = 152

Score = 142 bits (358), Expect = 4e-33

Identities = 67/136 (49%), Positives = 93/136 (68%), Gaps = 3/136 (2%)

Query: 76 WGCCPASWKSFGSSCYFIS--SEEKVVWSKSEQNCVEMGAHLVVFNTAEQNFIVQQLNES 133
W CCP W+ FGS CY + S W+KSE+NC MGAHLVV ++ EQ+FI L+

Sbjct: 18 WSCCPKDWRLFGSHCYLVPTVSSASWNKSEENC SRMGAHLVVIQSQEEQDFITGILDTH 77

Query: 134 FSYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSAEQCASIVFWKPTGWGWNDVI 193
+YF+GL D G+ WQW+D+TPYE+++ FWH GEP+ E+CA+I++ TGWGWND+

Sbjct: 78 AAYFIGLWD-TGHRQWQWVDQTPYEESITFWHNGEPSSGNEKCATIIYRWKTGWGWNDIS 136

Query: 194 CETRRNSICEMNKIYL 209
C ++ S+C+M KI L

Sbjct: 137 CSLKQKSVCQMCKINL 152

[gi|7657333|ref|NP_055173.1|](#) [C-type lectin, superfamily member 9; macrophage-](#)
[lectin \[Homo sapiens\]](#)

[gi|5821288|dbj|BAA83755.1|](#) [macrophage C-type lectin Mincle \[Homo sapiens\]](#)

[gi|12653849|gb|AAH00715.1|](#) [C-type lectin, superfamily member 9 \[Homo sapiens\]](#)

[gi|37182121|gb|AAQ88863.1|](#) CLECSF9 [Homo sapiens]
Length = 219

Score = 140 bits (353), Expect = 2e-32

Identities = 82/205 (40%), Positives = 118/205 (57%), Gaps = 5/205 (2%)

Query: 3 QEQQPQSTEKRGWLS-LRLWSVAGISIALLSACFIVSCVVTYHFTYGETGKRLSELHSYH 61
+ + Q TE+ + S + LW+VAGI I LSACFI CVVT+ + ++ +L

Sbjct: 5 KSSETQCTERGCFFSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPENF 63

Query: 62 SSLTCFSEGTKVPAWGCCPASWKSFGSSCYFISSEEKVVWSKSEQNCVEMGAHLVVFNTAE 121
+ L+C++ G+ CCP +W+ F SSCYF S++ W+ S +NC MGAHLVV N++

Sbjct: 64 TELSCYNYGSG-SVKNCCPLNWEYFQSSCYFFSTDITISWALS LKNCSAMGAHLVVINSQE 122



Query: 122 EQNFIVQQLNESFSYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHS--EQCASI 179
EQ F+ + + +F+GLSD WQW+D TP K++ FW +GEPN+ A E CA++

Sbjct: 123 EQEFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTP LTKSLSFWDVGEPNNIATLED CATM 182

Query: 180 VFWKPTGWGWNDVICETRRNSICEM 204

WNDV C ICEM

Sbjct: 183 RDSSNPRQNWNDVTCFLNYFRICEM 207

 >gi|34858417|ref|XP_342753.1|  similar to RIKEN cDNA 3110037K17 [Rattus norvegicus]
Length = 237

Score = 140 bits (352), Expect = 2e-32

Identities = 64/135 (47%), Positives = 91/135 (67%), Gaps = 2/135 (1%)

Query: 76 WGCCPASWKSFGSSCYFISSEE-KVWSKSEQNCVEMGAHLVVFNTAEQNFIVQQLNESF 134
W CCP WK F S+CYF S++ + W +SE+ C +GAHLVV +++ EQ+F+ + L+

Sbjct: 104 WSCCPKDWKPFDSNCFPSTDSVESWMESEKCSGIGAHLVVIHSQEEQDFLPRILDTHA 163



Query: 135 SYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSAEQCASIVFWKPTGWGWNDVIC 194
+YF+GLSDP G+ WQW+D+TPY N FWH GEP+ EQC I + TGWGW+D C

Sbjct: 164 AYFIGLSDP-GHRQWQWVDQTPYNGNATFWHEGEPSSDNEQCVIINHENTGWGWSDSSC 222

Query: 195 ETRRNSICEMNKIYL 209

++ +C++ KIIYL

Sbjct: 223 SDKQKLVCQVKKIYL 237

 >gi|34858419|ref|XP_232393.2|  similar to dendritic cell immunoreceptor [Rattus norvegicus]
Length = 767

Score = 137 bits (345), Expect = 1e-31

Identities = 65/134 (48%), Positives = 86/134 (64%), Gaps = 4/134 (2%)

Query: 71 TKVPAWGCCPASWKSFGSSCYFISSEK-VWSKSEQNCVEMGAHLVVFNTAEQNFIVQQ 129
T+ A CC WKSFGS CYF S++ K W +S++ C MGAHL+V +++ EQ+FI

Sbjct: 99 TEDKACSCCLKGWKSFGSYCYFTSTDSKATWDESKEKCSRMGHLLVIHSQDEQDFINTI 158

Query: 130 LNESFSYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSAEQCASIVFWKPTGWGW 189
LN YF+GLSD N WQWID+TPY ++V FWH GEPN+ E+C +V WGW

Sbjct: 159 LNIGTDYFIGLSD-HSENQWQWIDQTPYNESVTFWHKGEPPNNKEKC--VVINHRDKWGW 215

Query: 190 NDVICETRRNSICE 203

ND+ C R S+C+

Sbjct: 216 NDIPCHDRHKSVCQ 229

Score = 94.7 bits (234), Expect = 9e-19

Identities = 41/81 (50%), Positives = 54/81 (66%), Gaps = 1/81 (1%)

Query: 123 QNFIVQQLNESFSYFLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHSAEQCASIVFW 182
++FI L+ + YF GLSD QG N WQWID+TPY ++V FWH EPN+ E+C I

Sbjct: 503 EDFINGILDTRWGYFTGLSD-QGQNQWQWIDQTPYNESVTFWHEDEPNNDYEKCEINHH 561

Query: 183 KPTGWGWNDVICETRRNSICE 203

K GWGWND++C + SIC+

Sbjct: 562 KDIGWGWNDIVCSSEHKSICQ 582

Score = 47.0 bits (110), Expect = 2e-04

Identities = 22/33 (66%), Positives = 26/33 (78%)

Query: 41 VTYHFTYGETGKRLSELHSYHSSLTCFSEGTKV 73
 VTY FT + +RLSELH+YHSSLTC S+GT V
 Sbjct: 660 VTYQFTMEKPNRRLSELHTYHSSLTCCSKGTMV 692

Score = 37.7 bits (86), Expect = 0.12

Identities = 17/37 (45%), Positives = 24/37 (64%), Gaps = 1/37 (2%)

Query: 121 AEQNFIVQQLNESFSYFLGLSDPQGNNNWQWIDKTPY 157
 A ++FI LN +YF+GL D G+ WQW+ +TPY
 Sbjct: 382 AVRDFITGFLNRDAAYFIGLWD-SGHRQWQWVSQTPY 417

[gi|9910162|ref|NP_064332.1|](#) **L** C-type lectin, superfamily member 9 [Mus musculus]
[gi|5821286|dbj|BAA83754.1|](#) **L** macrophage C-type lectin Mincle [Mus musculus]
[gi|13096844|gb|AAH03218.1|](#) **L** C-type lectin, superfamily member 9 [Mus musculus]
 Length = 214

Score = 129 bits (323), Expect = 4e-29

Identities = 77/189 (40%), Positives = 110/189 (58%), Gaps = 5/189 (2%)

Query: 21 WSVAGISIALLSACFIVSCVVITYHFTYGETGKRLSELHSYHSSLTCFSEGTKVPAWGCCP 80
 W++AG SI LS CFI CVVTY + +G+ L + H L+C+SE + CCP
 Sbjct: 25 WTIAGASILFLSGCFITRCVVITYR-SSQISGQNL-QPHRNIKELSCYSEASG-SVKNCCP 81

Query: 81 ASWKSFGSSCYFISSEEEKVWSKSEQNCVEMGAHLVVFNTAEQNFIVQQLNESFSYFLGL 140
 +WK + SSCYF S+ WS S +NC +MGAHLVV +T+ EQ F+ + + +++GL
 Sbjct: 82 LNWKHYQSSCYFFSTTTLTWSSSLKNCSMDGAHLVVIDTQEEQEFLFRTKPKRKEFYIGL 141

Query: 141 SDPQGNNNWQWIDKTPYEKNVRFWHLGEPNHS--AEQCASIVFWKPTGWGWNVICETRR 198
 +D WQW+D TP+ +++ FW GEPN+ E CA+I + WND+ C
 Sbjct: 142 TDQVVEGQWQWDDTPFTESLSFWDAGEPNNIVLVEDCATIRDSSNSRKNWWDIPCFYSM 201

Query: 199 NSICEMNKI 207
 ICEM +I
 Sbjct: 202 PWICEMPEI 210

[gi|25392184|pir||JC7595](#) scavenger receptor with C-type lectin type I - human
[gi|13365515|dbj|BAB39147.1|](#) **L** scavenger receptor with C-type lectin type I [Homo]
 Length = 742



Score = 95.5 bits (236), Expect = 5e-19

Identities = 49/146 (33%), Positives = 78/146 (53%), Gaps = 14/146 (9%)

Query: 68 SEGTKVPAWGCCPASWSFGSSCYFISSEEEKVWSKSEQNCVEMGAHLVVFNTAEQNFIV 127
 +E T P CP WK+F CY+ S E++++ ++ C + +HLV NT EQ +I
 Sbjct: 596 NEPTAPEDNSCPPHWKNFTDKCYYSVEKEIFEDAKLFCEDKSSHLVFINTRREEQQWIK 655

Query: 128 QQLNESFSYFLGLSDPQGNNNWQWIDKT-PYEKNVRFWHLGEPNH-----SAEQCASIV 180
 +Q+ S+++GL+D + N W+W+D T P KN W G+P++ E CA ++
 Sbjct: 656 KQMVGRESHWIGLTDSERENEWKWDGTSPDYKN---WKAGQPDNWGHGHPGEDCAGLI 712

Query: 181 FWKPTGWWNDVICETRRNSICEMNK 206
 + WND CE N ICE ++
 Sbjct: 713 Y----AGQWDFQCEDVNNFICEKDR 734



 >gi|38174510|gb|AAH60789.1|  Collectin sub-family member 12, isoform I [Homo sa
 Length = 742

Score = 95.5 bits (236), Expect = 5e-19
 Identities = 49/146 (33%), Positives = 78/146 (53%), Gaps = 14/146 (9%)

Query: 68 SEGTKVPAWGCCPASWKSFGSSCYFISSEKVVWSKSEQNCVEMGAHLVVFNTAEQNFIV 127
 +E T P CP WK+F CY+ S E++++ ++ C + +HLV NT EQ +I
 Sbjct: 596 NEPTPAPEDNSCPPHWKNFTDKCYYSVEKEIFEDAKLFCEDKSSHLVFINTREEQQWIK 655

Query: 128 QQLNESFSYFLGLSDPQGNWQWIDKT-PYEKNVRFWHLGEPNH-----SAEQCASIV 180
 +Q+ S+++GL+D + N W+W+D T P KN W G+P++ E CA ++
 Sbjct: 656 KQMVGRESHWIGLTDSERENWKLWLDGTSPDYKN--WKAGQPDNWGHGHPGEDCAGLI 712


Query: 181 FWKPTGWWNDVICETRRNSICEMNK 206
 + WND CE N ICE ++
 Sbjct: 713 Y----AGQWDFQCEDVNNFICEKDR 734

 >gi|34858415|ref|XP_342752.1|  similar to C-type (calcium dependent, carbohydrate
 domain) lectin, superfamily member 6; dendritic cell
 immunoreceptor; C-type lectin [Rattus norvegicus]
 Length = 126

Score = 95.5 bits (236), Expect = 6e-19
 Identities = 43/118 (36%), Positives = 71/118 (60%), Gaps = 3/118 (2%)

Query: 94 SSEEKVVWSKSEQNCVEMGAHLVVFNTAEQNFIVQQLNESFSYFLGLSDPQGNWQWID 153
 + + WS SE+ C GAHL+V +++ EQ+FI LN Y++GLSD +G+ WQW+D
 Sbjct: 10 TGDSASWSDSEKCSHRGAHLLVIHSQEEQDFITDTLNPRAHYYVGLSDTEGHGKWQWVD 69

Query: 154 KTPYEKNVRFWHLGEPNHSAEQCASIVFWKPT--GWGWNDVICETRRNSICEMNKIYL 209
 +TP+ +N WH EP+ + C ++ + P GWGW+ C+ +C+M ++Y+
 Sbjct: 70 QTPFNQATSWHADEPSGNKGFCV-VLSYHPNLKGWGSVAPCDGYHRLVCKMRQLYV 126

 >gi|27356791|gb|AAL89528.1| putative CD209L1 protein [Hylobates lar]
 Length = 399

Score = 95.1 bits (235), Expect = 8e-19
 Identities = 51/128 (39%), Positives = 70/128 (54%), Gaps = 8/128 (6%)

Query: 79 CPASWKSFGSSCYFISSEKVVWSKSEQNCVEMGAHLVVFNTAEQNFIVQQLNESFSY-F 137
 CP W F +CYFIS+ ++ W S C E+GA LVV + EQNF+ Q + S + +
 Sbjct: 268 CPKDWTFQGNCFISNSQRNWHDSVTACREVGAGLVVVIKSAEEQNFLQLQSSRSNRFAW 327

Query: 138 LGLSDPQGNWQWIDKTPYEKNV-RFWHLGEPNHS-AEQCASIVFWKPTGWGWNDVICE 195
 +GLSD WQW+D +P + R+W+ GEPN+S E CA +G GWND C
 Sbjct: 328 MGLSDLNQEGTWQWVDGSPSSSFQRYWNSGEPNNSGDEDCAEF-----SGSGWNDNRCN 382

Query: 196 TRRNSICE 203

IC+

Sbjct: 383 VDNYWICK 390

>gi|18641360|ref|NP_569057.1| collectin sub-family member 12 isoform I; scavenger
C-type lectin; collectin placenta 1; scavenger receptor
class A, member 4 [Homo sapiens]

gi|17026101|dbj|BAB72147.1| collectin placenta 1 [Homo sapiens]
Length = 742

Score = 94.7 bits (234), Expect = 8e-19

Identities = 49/146 (33%), Positives = 78/146 (53%), Gaps = 14/146 (9%)

Query: 68 SEGTKVPAWGCCPASWKSFGSSCYFISSEKVVWSKSEQNCVEMGAHLVVFNTAEQNFIV 127
+E T P CP WK+F CY+ S E++++ ++ C + +HLV NT EQ +I

Sbjct: 596 NEPTPAPEDNGCPPHWKNFTDKCYFVSVEKEIFEDAKLFCEDKSSHLVFINTREEQQWIK 655

Query: 128 QQLNESFSYFLGLSDPQGNNNWQWIDKT-PYEKNVRFWHLGEPNH-----SAEQCASIV 180
+Q+ S+++GL+D + N W+W+D T P KN W G+P++ E CA ++

Sbjct: 656 KQMVGRESHWIGLTDSERENKWLDTGTSPTYKN--WKAGQPDNNGHGHGPGEDCAGLI 712

Query: 181 FWKPTGWGWNDVICETRRNSICEMNK 206

+ WND CE N ICE ++

Sbjct: 713 Y---AGQWDFQCEDVNNFICEKDR 734

>gi|27356800|gb|AAL89529.1| putative CD209L1 protein [Hylobates syndactylus]
Length = 422

Score = 94.7 bits (234), Expect = 9e-19

Identities = 50/128 (39%), Positives = 70/128 (54%), Gaps = 8/128 (6%)

Query: 79 CPASWKSFGSSCYFISSEKVVWSKSEQNCVEMGAHLVVFNTAEQNFIVQQLNESFSY-F 137
CP W F +CYF+S+ ++ W S C E+GA LVV + EQNF+ Q + S + +

Sbjct: 291 CPKDWTFQGNCFMSNSQRNWHDSVTACQEVGAQLVVIKSAEEQNFLQLQTSRNSNRFSW 350

Query: 138 LGLSDPQGNNNWQWIDKTPYEKNV-RFWHLGEPNHS-AEQCASIVFWKPTGWGWNDVICE 195
+GLSD WQW+D +P + R+W+ GEPN+S E CA +G GWND C

Sbjct: 351 MGLSDLNQEGTWQWVDGSPLSSSFQRYWNSGEPNNSGDEDCAEF-----SGSGWNDNRCN 405

Query: 196 TRRNSICE 203

IC+

Sbjct: 406 VDNYWICK 413

>gi|27356809|gb|AAL89530.1| putative CD209L1 protein [Hylobates concolor]
Length = 399

Score = 94.7 bits (234), Expect = 1e-18

Identities = 51/128 (39%), Positives = 70/128 (54%), Gaps = 8/128 (6%)

Query: 79 CPASWKSFGSSCYFISSEKVVWSKSEQNCVEMGAHLVVFNTAEQNFIVQQLNESFSY-F 137
CP W F +CYFIS+ ++ W S C E+GA LVV + EQNF+ Q + S + +

Sbjct: 268 CPKDWTFQGNCFISNSQRNWHDSVTACQEVGAQLVVIKSAEEQNFLQLQSSRSNRFTW 327

Query: 138 LGLSDPQGNNNWQWIDKTPYEKNV-RFWHLGEPNHS-AEQCASIVFWKPTGWGWNDVICE 195

+GLSD WQW+D +P + R+W+ GEPN+S E CA +G GWND C
 Sbjct: 328 MGLSDLNQEGTWQWVDGSPSSSFQRYWNSGEPNNSGDEDCAEF-----SGSGWNDNRNCN 382

Query: 196 TRRNSICE 203

IC+

Sbjct: 383 VDNWICK 390

☐ >gi|12084795|gb|AAG13815.2| ☒ probable mannose binding C-type lectin DC-SIGNR [Homo sapiens]
 gi|15383606|gb|AAK91859.1| mDC-SIGN2 type I isoform [Homo sapiens]
 gi|24416563|gb|AAH38851.1| ☒ CD209L protein [Homo sapiens]
 Length = 399

Score = 93.6 bits (231), Expect = 2e-18

Identities = 50/128 (39%), Positives = 70/128 (54%), Gaps = 8/128 (6%)

Query: 79 CPASWKSFGSSCYFISSEKVVSKSEQNCVEMGAHLVVFNTAEQNFIVQQLNESFSY-F 137
 CP W F +CYF+S+ ++ W S C E+ A LVV T EQNF+ Q + S + +
 Sbjct: 268 CPKDWTFQGNCFMSNSQRNWHDSVTACQEVRAQLVVIKTAEEQNFLQLQTSRNSNRFSW 327

Query: 138 LGLSDPQGNWQWIDKTPYEKNV-RFWHLGEPNHS-AEQCASIVFWKPTGWGWNDVICE 195
 +GLSD WQW+D +P + R+W+ GEPN+S E CA +G GWND C+
 Sbjct: 328 MGLSDLNQEGTWQWVDGSPSPSFQRYWNSGEPNNSGNEDCAEF-----SGSGWNDNRCD 382

Query: 196 TRRNSICE 203

IC+

Sbjct: 383 VDNWICK 390

☐ >gi|20149606|ref|NP_055072.2| ☒ CD209 antigen-like; putative type II membrane protein [Homo sapiens]
 gi|13383470|gb|AAK20998.1| ☒ L-SIGN [Homo sapiens]
 Length = 376

Score = 92.8 bits (229), Expect = 3e-18

Identities = 50/128 (39%), Positives = 70/128 (54%), Gaps = 8/128 (6%)

Query: 79 CPASWKSFGSSCYFISSEKVVSKSEQNCVEMGAHLVVFNTAEQNFIVQQLNESFSY-F 137
 CP W F +CYF+S+ ++ W S C E+ A LVV T EQNF+ Q + S + +
 Sbjct: 245 CPKDWTFQGNCFMSNSQRNWHDSVTACQEVRAQLVVIKTAEEQNFLQLQTSRNSNRFSW 304

Query: 138 LGLSDPQGNWQWIDKTPYEKNV-RFWHLGEPNHS-AEQCASIVFWKPTGWGWNDVICE 195
 +GLSD WQW+D +P + R+W+ GEPN+S E CA +G GWND C+
 Sbjct: 305 MGLSDLNQEGTWQWVDGSPSPSFQRYWNSGEPNNSGNEDCAEF-----SGSGWNDNRCD 359

Query: 196 TRRNSICE 203

IC+

Sbjct: 360 VDNWICK 367

☐ >gi|19584340|emb|CAD28466.1| ☒ hypothetical protein [Homo sapiens]
 Length = 417


Score = 92.4 bits (228), Expect = 4e-18

Identities = 49/146 (33%), Positives = 78/146 (53%), Gaps = 14/146 (9%)

Query: 68 SEGTKVPAWGCCPASWKSFGSSCYFISSEKVVWSKSEQNCVEMGAHLVVFNTAEQNFIV 127
 +E T P CP WK+F CY+ S E++++ ++ C + +HLV NT EQ +I
 Sbjct: 271 NEPTPAPEDNGCPPHWKNFTDKCYFVSVEKEIFEDAKLFCEDKSSHLVFINTRREEQQWIK 330

Query: 128 QQLNESFSYFLGLSDPQGNNNWQWIDKT-PYEKNVRFWHLGEPNH-----SAEQCASIV 180
 +Q+ S+++GL+D + N W+W+D T P KN W G+P++ E CA ++
 Sbjct: 331 KQMVGRESHWIGLTDSERENEWKWLDTSPDYKN---WKAGQPDNWGHGHGPGEDCAGLI 387

Query: 181 FWKPTGWGWNDVICETRRNSICEMNK 206
 + WND CE N ICE ++
 Sbjct: 388 Y----AGQWNDFQCEDVNNFICEKDR 409



 >gi|27356856|gb|AAL89536.1| putative CD209L1 protein [Pan troglodytes]
 Length = 445

Score = 92.0 bits (227), Expect = 6e-18
 Identities = 49/128 (38%), Positives = 70/128 (54%), Gaps = 8/128 (6%)

Query: 79 CPASWKSFGSSCYFISSEKVVWSKSEQNCVEMGAHLVVFNTAEQNFIVQQLNESFSY-F 137
 CP W F +CYF+S+ ++ W S C E+ A LVV + EQNF+ Q + S + +
 Sbjct: 314 CPKDWTFQGNCFMNSQRNWHNSVTACREVRAQLVVIKSAAEQNFLLQLQTSRNSNRFSW 373

Query: 138 LGLSDPQGNNNWQWIDKTPYEKNV-RFWHLGEPNHS-AEQCASIVFWKPTGWGWNDVICE 195
 +GLSD WQW+D +P + R+W+ GEPN+S E CA +G GWND C+
 Sbjct: 374 MGLSDLNQEGTWQWVDGSPSPSFQRYWNSGEPNNSGNEEDCAEF-----SGSGWNDNRCD 428

Query: 196 TRRNSICE 203
 IC+
 Sbjct: 429 IDNYWICK 436


 >gi|15383614|gb|AAK91863.1|  sDC-SIGN2 type I isoform [Homo sapiens]
 Length = 332

Score = 91.3 bits (225), Expect = 9e-18
 Identities = 50/128 (39%), Positives = 70/128 (54%), Gaps = 8/128 (6%)

Query: 79 CPASWKSFGSSCYFISSEKVVWSKSEQNCVEMGAHLVVFNTAEQNFIVQQLNESFSY-F 137
 CP W F +CYF+S+ ++ W S C E+ A LVV T EQNF+ Q + S + +
 Sbjct: 201 CPKDWTFQGNCFMNSQRNWHNSVTACQEVRAQLVVIKTAAEQNFLLQLQTSRNSNRFSW 260

Query: 138 LGLSDPQGNNNWQWIDKTPYEKNV-RFWHLGEPNHS-AEQCASIVFWKPTGWGWNDVICE 195
 +GLSD WQW+D +P + R+W+ GEPN+S E CA +G GWND C+
 Sbjct: 261 MGLSDLNQEGTWQWVDGSPSPSFQRYWNSGEPNNSGNEEDCAEF-----SGSGWNDNRCD 315

Query: 196 TRRNSICE 203
 IC+
 Sbjct: 316 VDNYWICK 323

 >gi|18157520|dbj|BAB83835.1| supported by GENSCAN and partially homologous to the
 domain [Oryzias latipes]
 Length = 236


Score = 91.3 bits (225), Expect = 9e-18

Identities = 53/132 (40%), Positives = 69/132 (52%), Gaps = 9/132 (6%)

Query: 79 CPASWKSFGSSCYFISSEKVVWSKSEQNCVEMGAHLVVFNTAEQNFIVQQLNESF--SY 136
CP +W F SSCYFIS++ K W S+ C GAHL + +T EQ F+ L + +Y
Sbjct: 101 CPTNWHLFNSSCYFISTQMKPWRDSQTYCQRQGAHLAIHTAEEQTFWLWDLPLRAHWNAY 160

Query: 137 FLGLSDPQGNNNWQWIDKTPYEKNVRFWHLGEP-NHSAEQCASI---VFWKPTGWGWND 191
+ G+SD Q + W+W+D T EK+ FW GEP NH E C I V + W D
Sbjct: 161 WFGISDRQKEDEWKWVDGTSVEKS--FWEEGEPNNHINEDCGYIVKTQVLERVAIRSWYD 218

Query: 192 VICETRRNSICE 203
CE ICE
Sbjct: 219 APCEMSIKFICE 230

 >gi|27356845|gb|AAL89534.1| putative CD209L1 protein [Gorilla gorilla]
Length = 376



Score = 91.3 bits (225), Expect = 9e-18

Identities = 49/128 (38%), Positives = 70/128 (54%), Gaps = 8/128 (6%)

Query: 79 CPASWKSFGSSCYFISSEKVVWSKSEQNCVEMGAHLVVFNTAEQNFIVQQLNESFSY-F 137
CP W F +CYF+S+ ++ W S C E+ A LVV + EQNF+ Q + S + +
Sbjct: 245 CPKDWTFFQGNCFMSNSQRNWHNSVTACQEVRAQLVVIKSAEEQNFLQLQTSRNSRFSW 304

Query: 138 LGLSDPQGNNNWQWIDKTPYEKNV-RFWHLGEPNHSA-EQCASIVFWKPTGWGWNDVICE 195
+GLSD WQW+D +P + R+W+ GEPN+S E CA +G GWND C+
Sbjct: 305 MGLSDLNQEGTWQWVDGSPLSPSFQRYWNSGEPNNSGNEDCAEF-----SGSGWNDNRCD 359

Query: 196 TRRNSICE 203
IC+
Sbjct: 360 VDNYWICK 367

 >gi|34870124|ref|XP_344065.1|  similar to SIGNR3 [Rattus norvegicus]
Length = 212


Score = 90.9 bits (224), Expect = 1e-17

Identities = 48/127 (37%), Positives = 67/127 (52%), Gaps = 7/127 (5%)

Query: 79 CPASWKSFGSSCYFISSEKVVWSKSEQNCVEMGAHLVVFNTAEQNFIVQQLNESFSYFL 138
CP W F SCYF S ++ W S C E+GA LV+ T+ EQ F+ Q ++
Sbjct: 81 CPRDWTFFNGSCYFFSKSQRNWHNSITACKELGAQLVIVETDEEQTFLLQQTSTKTRGPTWM 140

Query: 139 GLSDPQGNNNWQWIDKTPYEKN-VRFWHLGEPNHSA-EQCASIVFWKPTGWGWNDVICET 196
GLSD W W+D +P + ++W+ GEPN+ E CA +G GWND+ C+T
Sbjct: 141 GLSDMHNEATWHWVDGSPLSPSFAQYWNRGEPNNVGDEDCAEF-----SGDGWNDLRCDT 195

Query: 197 RRNSICE 203
R IC+
Sbjct: 196 RIFWICK 202

 >gi|27356883|gb|AAL89539.1| putative CD209 protein [Hylobates syndactylus]
Length = 381

Score = 90.5 bits (223), Expect = 2e-17

Identities = 49/130 (37%), Positives = 73/130 (56%), Gaps = 8/130 (6%)

Query: 79 CPASWKSFGSSCYFISSEKVVWSKSEQNCVEMGAHLVVFNTAEQNFIVQQLNESFSY-F 137
CP W F +CYF+S+ ++ W S C E+GA LVV + EQNF+ Q + S + +
Sbjct: 233 CPWEWTFQNGCYFMSNSQRDWQDSVTACQEVGAQLVVIKSAEEQNFLQLQSSRSNRFAW 292

Query: 138 LGLSDPQGNWQWIDKTPYEKNVR-FWHLGEPNHSAEQ-CASIVFWKPTGWGWNDVICE 195
+GLSD WQW+D +P + + +W+ GEPN+ E+ CA +G GWND C
Sbjct: 293 MGLSDVNQEGTWQWVDGSPLSPSFKHYWNRGEPNNIGEEDCAEF-----SGNGWNDKCN 347

Query: 196 TRRNSICEMN 205

+ IC+M+

Sbjct: 348 HAKFWICKMS 357

☐ >gi|27356854|gb|AAL89535.1| putative CD209L1 protein [Pan troglodytes]
Length = 445

Score = 90.5 bits (223), Expect = 2e-17

Identities = 48/128 (37%), Positives = 70/128 (54%), Gaps = 8/128 (6%)

Query: 79 CPASWKSFGSSCYFISSEKVVWSKSEQNCVEMGAHLVVFNTAEQNFIVQQLNESFSY-F 137
CP W F +CYF+S+ ++ W S C E+ A LVV + EQNF+ Q + S + +
Sbjct: 314 CPKDWTFQNGCYFMSNSQRNWHNSVTACREVRAQLVVIKSAEEQNFLQLQTSRSNRFSW 373

Query: 138 LGLSDPQGNWQWIDKTPYEKNVR-FWHLGEPNHSAEQ-CASIVFWKPTGWGWNDVICE 195
+GLSD WQW+D +P + + +W+ GEPN+S E CA +G GWND C+
Sbjct: 374 MGLSDLNQEGLTWQWVDGSPLSPSFQXYWNSGEPNNSGNEDCAEF-----SGSGWNDNRCD 428

Query: 196 TRRNSICE 203

IC+

Sbjct: 429 IDNYWICK 436

☐ >gi|12084797|gb|AAG13848.2| ☒ probable mannose binding C-type lectin DC-SIGNR [H
Length = 399

Score = 90.1 bits (222), Expect = 2e-17

Identities = 47/127 (37%), Positives = 70/127 (55%), Gaps = 6/127 (4%)

Query: 79 CPASWKSFGSSCYFISSEKVVWSKSEQNCVEMGAHLVVFNTAEQNFIVQQLNESFSY-F 137
CP W F +CYF+S+ ++ W S C E+ A LVV T EQNF+ Q + S + +
Sbjct: 268 CPKDWTFQNGCYFMSNSQRNWHNSVTACQEVRAQLVVIKTAEQNFLQLQTSRSNRFSW 327

Query: 138 LGLSDPQGNWQWIDKTPYEKNV-RFWHLGEPNHSAEQ-CASIVFWKPTGWGWNDVICET 196
+GLSD WQW+D +P + R+W+ GEPN+S + + +G GWND C+
Sbjct: 328 MGLSDLNQEGLTWQWVDGSPLSPSFQRYWNSGEPNNSGNEDXA----EFSGSGWNDNRCDV 383

Query: 197 RRNSICE 203

IC+

Sbjct: 384 DNYWICK 390

☐ >gi|27356874|gb|AAL89538.1| putative CD209 protein [Hylobates lar]

Length = 450

Score = 89.4 bits (220), Expect = 4e-17

Identities = 48/128 (37%), Positives = 71/128 (55%), Gaps = 8/128 (6%)

Query: 79 CPASWKSFGSSCYFISSEKVVWSKSEQNCVEMGAHLVVFNTAEQNFIVQQLNESFSY-F 137
CP W F +CYF+S+ ++ W S C E+GA LVV + EQNF+ Q + S + +

Sbjct: 302 CPWEWTFQGNCFMSNSQRDWHDSVTACQEVGAQLVVIKSAEEQNFLQLQSSRSNRFAW 361

Query: 138 LGLSDPQGNNNWQWIDKTPYEKNVR-FWHLGEPNHSAEQ-CASIVFWKPTGWGWNDVICE 195
+GLSD WQW+D +P + + +W+ GEPN+ E+ CA +G GWND C

Sbjct: 362 MGLSDLNQEGTWQWVDGSPLSPSFKQYWNRGEPNNVGEEEDCAEF-----SGNGWNDDKCN 416

Query: 196 TRRNSICE 203

+ IC+

Sbjct: 417 LAKFWICK 424

Get selected sequences

Select all

Deselect all

Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF

Posted date: Jan 26, 2004 1:24 AM

Number of letters in database: 530,365,172

Number of sequences in database: 1,612,710

Lambda	K	H
0.319	0.132	0.446

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 46,303,767

Number of Sequences: 1612710

Number of extensions: 1858764

Number of successful extensions: 4428

Number of sequences better than 10.0: 250

Number of HSP's better than 10.0 without gapping: 136

Number of HSP's successfully gapped in prelim test: 114

Number of HSP's that attempted gapping in prelim test: 4087

Number of HSP's gapped (non-prelim): 291

length of query: 209

length of database: 530,365,172

effective HSP length: 119

effective length of query: 90

effective length of database: 338,452,682

effective search space: 30460741380

effective search space used: 30460741380

T: 11

A: 40

X1: 16 (7.4 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)
S1: 41 (21.8 bits)
S2: 70 (31.6 bits)